

GENERAL AND SPECIFIC COMBINING ABILITY STUDIES OF SELECTED TROPICAL WHITE MAIZE INBRED LINES FOR YIELD AND YIELD RELATED TRAITS

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ABSTRACT

In Ghana: low yield of maize 1.7 t ha⁻¹ has been reported. Thus, use inbred lines with good combining ability for yield and yield-contributing characters to form excellent combinations is crucial. Thus, the present study was designed to estimate the combining ability effects of tropical white maize inbred lines for yield and yield-contributing traits. A line x tester mating design involving sixteen white maize inbred lines as females and two testers as males generated thirty-two single crosses. These hybrids plus three checks were evaluated using a 5 x 7 alpha lattice design replicated twice at the University of Ghana, WACCI research farm during 2015/16 off-season using drip irrigation. Analysis of variance revealed that genotype mean squares were highly significant ($P \leq 0.001$) for days to 50% anthesis and silking, plant and ear height, plant aspect, ear length, number of kernel rows ear⁻¹, number of kernels row⁻¹ and yield. Similarly, mean squares of genotypes were significant ($p \leq 0.05$) for ear rots, anthesis-silking interval, husk cover and maize streak virus disease. Line x tester revealed both additive and non-additive gene action played important role in the inheritance of all the traits indicating that both progeny selection and heterosis breeding will be valuable for future breeding programme using these inbred lines. However, the ratio of general combining ability (GCA) variance to specific combining ability (SCA) variance was less than unity, indicating the prevalence of non-additive gene action in the inheritance of all the parameters studied except for days to 50% anthesis and anthesis-silking interval

Three inbred lines L16 (867), L1 (595) and L8 (247) were identified to have high GCA effects for yield kg ha⁻¹, indicating that these lines have the genetic potential to transmit this desirable trait to their progenies. Based on the SCA effect for grain yield, the lines were separated into two heterotic groups. The lines L1, L3, L4, L8, L11 and L14 belonged to tester group 1368 while L2, L5, L6, L7, L9, L10, L12, L13, L15 and L16 belonged to heterotic group of CML 444. This is useful for the development of hybrids and synthetic varieties. The information generated in the present study will be useful for breeders who want to improve yield and yield-contributing traits of maize.

KEYWORDS: Heterotic Group, GCA, Inbred Line, Line X Tester & SCA

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INTRODUCTION

Maize (*Zea mays* L., $2n = 2x = 20$) is a significant cereal crop of the world, belonging to the tribe Maydeae of the grass family *Poaceae*. Maize has a wide adaptation across diverse agro-ecologies. It is an important food security crop for millions of people in the developing world, especially in sub-Saharan Africa (SSA) and Latin America (Shiferaw *et al.*, 2011). It is ranked 3rd in the world after wheat and rice in terms of total area planted. The estimated area under maize production in the world is 184192053 ha, with an average yield of

5.51998 t ha⁻¹ whilst in Africa it produced on 35019749 ha with average yield of 2.0449 t ha⁻¹ (FAOSTAT, 2013). About 20 % of the area harvested is in SSA (FAOSTAT, 2013) where maize is widely grown for direct human consumption.

A crucial objective of maize breeding programmes is to develop and use inbred lines with good combining ability for yield and yield-contributing characters to form excellent combinations (Menkir *et al.*, 2003a; Amiruzzaman *et al.*, 2010; Amin *et al.*, 2014; Chandel, 2014). According to Allard (1960) and Griffing (1956) parents transmit genes, not genotypes, to their progenies. The average effects of the parent's genes determine the genotypic value of its offspring (Makumbi, 2005; Gomes *et al.*, 1995). Therefore, the value of parent is estimated by the mean performance of its progeny and progeny selection is one of the key steps of plant breeding programmes.

To make effective use of the available genetic materials and to develop high yielding maize hybrid varieties, information on combining abilities are desirable (Menkir *et al.*, 2003b; Legesse *et al.*, 2009; Librando *et al.*, 2008; Vasal *et al.*, 1992; Khalil *et al.*, 2010). Such information gives an indication on the nature of gene action involved in controlling quantitative traits to assist breeders in selecting promising parental lines (Hallauer *et al.*, 1988; Vasal *et al.*, 1992b). Several approaches are available for this selection, the key criteria used by many researchers is combining ability, which can be classified as general or specific (Sprague and Tatum, 1942). The general combining ability (GCA) is related to additive genetic effects, while specific combining ability (SCA) is related to dominance and epistatic effects (non-additive effects) of the genes. Thus, information on GCA effects can aid breeders to exploit existing variability in breeding materials to choose genotypes having desirable attributes and to distinguish relatedness among the breeding materials (Ai-Zhi *et al.*, 2012; Matta, 2003; Sprague and Tatum, 1942). The SCA effects help breeders to determine heterotic patterns among populations or inbred lines to identify promising single crosses and assign them into heterotic groups (Menkir *et al.*, 2004; Vasal *et al.*, 1992a and 1992b). Thus, knowledge on combining ability effects aids the breeder in selecting the desirable parental lines with high GCA effects and crosses with high SCA values

The line × tester analysis technique which was recommended by Kempthorne (1957) is one of the effective techniques available to estimate GCA and SCA effects and assists in selecting desirable parental lines and crosses and or effective deciding the relative ability of female and male lines to produce the best hybrid combinations. When numerous of maize inbred lines are present in a breeding programme breeders cannot estimate the combining ability of inbred lines in a diallel mating design because the number is prohibitive (Menkir, 2003a; Vasal *et al.*, 1999). Line x tester analysis also renders information on genetic components and aids the breeder to choose suitable breeding methods for high yielding hybrid variety development programmes.

The West Africa Center for Crop improvement (WACCI) maize research programme has a number of inbred lines from various sources. So far, no information is available on these new inbred lines on the GCA effects of the lines and the SCA effects of their hybrid combinations

The objective of the study was to: estimate the combining ability effects of tropical white maize inbred lines for yield and yield-contributing traits.

MATERIAL AND METHODS

Description of Experimental Area

The experiment was carried out during 2015/16 offseason using drip irrigation at, West Africa Centre for Crop Improvement research field, University of Ghana. The University is located at 5.6508° N, latitude and 0.1869° W longitude

and an altitude 97 meter above sea level (m.a.s.l).

Genetic Materials used for the Study

Eighteen white tropical maize inbred lines with diverse genetic backgrounds were selected from the pool of inbred lines at the West Africa Centre for Crop Improvement (WACCI). This comprises of ten lines from the International Institute for Tropical Agriculture (IITA), six from International Maize and Wheat improvement Center (CIMMYT) and the two testers 1368 from IITA and CML 444 from CIMMYT maize breeding programmes. The 16 inbred lines were crossed to the two testers using the line by tester method (Table 1) and it generated 32 (16 x 2) cross combinations.

Table 1: List of Parents and Testers used for the Study

Code No.	Female parents	Male parents	
		1368 (T1)	CML 444 (T2)
L1	TZMI 763	X	X
L2	TZMI746	X	X
L3	TZMI749	X	X
L4	CML15	X	X
L5	CML 24	X	X
L6	TZMI740	X	X
L7	CML16	X	X
L8	TZMI-Unknown	X	X
L9	TZ-STR-133	X	X
L10	TZIL41	X	X
L11	CML10	X	X
L12	9006	X	X
L13	CML 05	X	X
L14	TZIL 39	X	X
L15	CML12	X	X
L16	TZMI760	X	X

Experimental Design and Field Evaluation

The 32 F₁ crosses including the hybrids between the two testers, one popular open pollinated variety and a standard hybrid checks were evaluated for their agronomical performance using a 5 x 7 alpha lattice designs at WACCI research field, the University of Ghana under irrigation system during 2015/2016. The genotypes were planted in two- rows plots, 5m long with spacing of 0.75 m between rows and 0.5 m spacing between plants within a row. Three seeds were planted per hill, and then thinned to two plants per hill after three weeks of planting, giving 22 plants per row or 44 plants plot⁻¹, to get a total plant density of 53333 plants ha⁻¹. The experiment was managed using normal agronomic practices (planting, irrigation, thinning, fertilization, weeding and insect controls) from sowing to maturity.

Grain Yield was computed from field weight (kg ha⁻¹), adjusted to 15% moisture content and 80% shelling percentage as follows.

$$\text{Grain yield (kg ha}^{-1}\text{)} = \frac{\text{Fresh ear weight (kg plot}^{-1}\text{)} \times (100 - \text{MC}) \times 0.8 \times 10000}{(100 - 15) \times \text{Area harvested (plot size)}}$$

$$\text{Fresh ear weight} = \text{Fresh weight of the cob row}^{-1}$$

$$0.8 = \text{Shelling coefficient}$$

$$85 = \text{Standard value of grain moisture at 15\%}$$

MC = Moisture content (%) in grains at harvest

Statistical Analysis

Data Analysis and Procedures

Analysis of variance for all agronomic parameters studied was calculated using the PROC GLM procedure and test for significant differences among the genotypes was performed using SAS software (SAS, 2002). Traits that showed significant differences among genotypes were further partitioned into crosses, checks and check vs crosses using (SAS, 2002). Traits that showed significant differences among crosses were partitioned into three components, namely females in crosses, males in crosses and female x male in crosses (Kempthorne, 1957; Singh and Chaudhary, 1985). The crosses means were adjusted for block effects as analyzed according to lattice design (Singh and Chaudhary, 1985) and used to perform combining ability analysis.

Combining Ability Analysis

Analysis of variance for line x tester without checks was performed to estimate general combining ability (GCA) and specific combining ability (SCA) effects based on the method described by Singh and Chaudhary, (1985) ; Kempthorne, (1957). Accordingly, contributions of females, males and their interaction to the hybrids was ascertained with the following models

$Y_{ijk} = G + g_i + g_j + s_{ij} + e_{ij}$, Where; Y_{ijk} = performance of the hybrid when i^{th} line is crossed to j^{th} tester, G = overall mean, g_i = general combining ability of i^{th} line, g_j = general combining ability of the j^{th} tester, while s_{ij} = specific combining ability (SCA) when i^{th} line is crossed to j^{th} tester and e_{ij} = random error term for ijk^{th} observation. Thus, the formula below was used for general combining ability (GCA) and specific combining ability (SCA) effects, as described by Singh and Chaudhary (1985) as shown below

GCA Effect

GCA effects of lines (g_i) and tester (g_j) were calculated as follows:

$$\text{Lines} = \text{GCA (line)} = g_i = \frac{\sum X_{i...}}{l} - \bar{X}$$

tr ltr

$$\text{Testers} = \text{GCA (line)} g_j = \frac{\sum X_{.j.}}{l} - \bar{X}$$

lr ltr

Where

g_i = GCA effect for i^{th} line

g_j = GCA effect for j^{th} tester

$X_{.j.}$ = sum of the j^{th} tester

$X_{i...}$ = Sum of the i^{th} line

\bar{X} = grand sum

l = number of lines

T= number of testers

R = number of replications

SCA Effect

$$\text{SCA effect} = S_{ij} = x_{ij} - \bar{x}_{i.} - \bar{x}_{.j} + \bar{x}_{..}$$

r tr lr ltr

Where,

S_{ij} = SCA effect of the ij^{th} crosses

$X_{ij.}$ = i x j cross sum

Standard Errors for Combining Ability Effects Were Calculated as

- **Standard error for general combining ability effects**

- **Line:** SE (GCA for line) = $(MSe/rt)^{1/2}$

- **Tester:** SE (GCA of tester) = $(MSe/rl)^{1/2}$

- **Standard error for specific combining ability effects**

$$SE (\text{SCA effects}) = (MSe/r)^{1/2}$$

- **Standard Error of the Difference between Combining Ability Effects**

- Standard error of the differences between general combining ability effects

$$SE (g_i - g_j) \text{ lines} = (2MSe/rt)^{1/2}$$

$$SE (g_i - g_j) \text{ testers} = (2MSe/rl)^{1/2}$$

- standard error of the difference between specific combining ability effects

$$SE (S_{ji} - S_{ki}) = (2MSe/r)^{1/2}$$

The significant of GCA and SCA effects were tested by dividing the corresponding GCA and SCA values by their respective standard errors and comparing the obtained t with tabular t- values at error degree of freedom using SAS and Excel Microsoft.

Combining Ability Variances

$$\text{Variance of GCA} = [(MSI - MS_{Ixt}) + (MSt - MS_{Ixt})] / [r (1+t)]$$

$$\text{Variance of SCA} = [MS_{Ixt} - MSe] / r$$

Proportional Contribution of lines, testers and their interaction line × tester to the total variances of crosses were calculated as follows:

The contribution

$$\text{Due to Lines} = \frac{\text{SS due to lines}}{\text{SS due to crosses}} \times 100$$

SS due to crosses

The contribution

$$\text{Due to Testers} = \frac{\text{SS due to testers}}{\text{SS due to crosses}} \times 100$$

SS due to crosses

The contribution due to

$$\text{Line} \times \text{Tester} = \frac{\text{SS due to tester L} \times \text{T}}{\text{SS due to crosses}} \times 100$$

SS due to crosses

Where, SS is sum squares due to lines, testers, line by tester and crosses

Line x Tester Analysis

The result showed that mean squares of GCA for lines were highly significant at $P \leq 0.001$, for days to 50% anthesis and silking, plant height, ear height, plant aspect, ear length, number of kernel rows ear⁻¹, and number of kernels row⁻¹. Highly significant differences at $P \leq 0.01$ were detected for anthesis-silking interval, maize streak virus disease, ear rot and grain yield. In addition, significant differences ($P \leq 0.05$) were observed for husk cover.

The mean squares due to GCA for testers were significant $P \leq 0.001$, for days to 50% anthesis and ear length, significant at $P \leq 0.01$ were mean squares for anthesis-silking interval, plant aspect and number of kernel rows ear⁻¹, and significant at $P < 0.05$ were days to 50% silking, plant and ear height. The GCA mean squares for testers were not significant for husk cover, ear rot and number of kernels row⁻¹.

The line x tester (SCA) mean squares showed significant differences at $p \leq 0.001$ for plant height, ear length and number of kernels row⁻¹, and significant differences at $P \leq 0.05$ for days to 50% silking, ear height, number of kernel rows ear⁻¹ and grain yield. No significant differences for days to 50% anthesis, anthesis-silking interval, plant aspect, maize streak virus disease score, husk cover and ear rot.

Table 2: Mean Square of Genotypes, Crosses, Crosses vs Check, Lines, Testers and Line X Testers for Grain Yield and Yield Contributed Traits of Maize at University of Ghana, WACCI Research Farm in 2015/16

Source of Var.	DF	AD	SD	ASI	MSD	PH	EH	PLASP
Rep	1	2.41*	0.91	0.23	0.32	73.64	10.73	0.13
B(rep)	12	2.97***	2.70***	0.18	0.08	185.38***	75.13*	0.39
Genotype (G)	34	4.00***	3.76***	1.06*	0.35*	320.39***	147.56***	0.97***
Crosses (Cr)	31	4.34***	3.84***	0.79*	0.25*	220.16***	130.26***	0.89***
Checks (Ch)	2	3.50	0.67	1.17	1.04	2233.04	765.25	1.17
Ch vs. Cr	1	0.41	8.01	11.41***	2.17**	1189.44*	39.23	3.68*
Lines (L)	15	7.03***	6.23***	1.10*	0.35**	268.68***	153.84***	1.00***
Testers (T)	1	12.60***	2.11*	4.71**	0.02	199.12*	184.63*	1.91**
L x T	15	0.57	0.94*	0.18	0.16	154.15***	78.38*	0.40
Pooled error (G)	22	0.56	0.39	0.44	0.17	33.68	30.01	0.21
Pooled error (Cr)	19	0.53	0.41	0.36	0.11	31.78	30.68	0.19
Pooled error (Ch)	2	1.50	2.00	0.50	0.21	269.55	50.73	0.17

*, ** and ***=Mean squares significant at $P \leq 0.05$, $P \leq 0.01$ and $P \leq 0.001$, respectively

DF= Degree of freedom, Rep = replications, B(rep) = block within replications, AD = days to anthesis, SD = days to silking, ASI = an thesis- silking interval, MSD=maize streak disease, PH= plant height, EH= ear height, plAsp= plant aspect,

Table 2: Continued

Sor. Variation	DF	Combining ability variances					
		HC%	E rot%	EL	NKRE	NKR	Yld kg ha ⁻¹
Rep	1	0.53	1390.45***	2.41	0.06	10.4	219.73
B(rep)	12	30.87	80.53	0.96	1.10	6.36	484481.53*
Genotype (G)	34	214.29***	231.58***	6.27***	4.50***	27.6***	821052.27***
Crosses (Cr)	31	211.54***	206.54**	6.51***	4.24***	28.6***	814413.02***
Checks (Ch)	2	211.25	915.46	0.67	6.50	1.50	140967.46
Ch vs. Cr	1	247.88	347.82	0.13	0.83	3.67	2243241.61*
Lines (L)	15	303.97***	301.19***	7.31***	6.07***	28.1***	958743.06***
Testers (T)	1	0.67	189.95	18.0***	8.05**	5.86	1558855.12**
L x T	15	128.40*	109.63	3.85***	2.39*	25.9 ***	466294.02*
Pool error (G)	22	53.88	59.86	0.8	1.04	3.44	216747.25
Pool error (Cr)	19	48.54	64.02	0.8	0.94	3.52	207179.20
Pool error (Ch)	2	65.26	86.69	0.67	1.17	7.17	61967.87

HC% = husk cover, RL%= root lodging, SL%= shoot lodging, E rot= number ear rot, EL =ear length, NKRE = number of rows ear⁻¹, NKR =number of kernels row⁻¹ and Yld kgha⁻¹ = grain yield kg ha⁻¹

Proportional Contribution of Lines, Testers and Line X Testers

The proportional contribution of lines, testers and their interaction to the total variance of crosses are given in Table 4. **Due to Lines:** Lines contributed to the variation observed for days to 50% an thesis and silking, an thesis-silking interval, plant and ear height, ear length, number of kernels row⁻¹, number of kernel rows ear⁻¹ and grain yield.

Due to Testers: The contribution the testers to the variation observed among crosses was lowest for all traits for days to 50% an thesis and an thesis- silking interval.

Due to Line x Tester: The contribution to the variation observed among crosses varied from low to moderate. However, the result revealed that most the genetic contributions for the studied traits came from the female lines. Thus, genetic contribution due to line x tester interaction was lower than lines for all traits but higher than contribution of testers.

Table 3: Proportional Contribution of Lines, Testers and Line X Testers to the Total Variance of Testcrosses and Combining Ability Variances

Traits	Contribution (%)			Combining ability variances		
	Lines	Testers	Line x tester	σ^2_{gca}	σ^2_{Sca}	$\sigma^2_{gca}/\sigma^2_{Sca}$
AD	78.50	9.37	6.31	0.52	0.02	26.00
SD	78.42	1.77	11.80	0.21	0.27	0.78
ASI	67.41	19.16	11.27	0.14	0.09	1.56
MSD	67.22	0.25	30.00	0.004	0.05	0.08
PH	59.05	2.92	19.23	11.23	61.19	0.18
EH	57.14	4.57	29.12	7.70	23.85	0.32
PlAsp	54.62	6.93	22.02	0.07	0.11	0.64
Hc%	69.57	0.01	29.39	5.74	34.73	0.17
E rot	70.35	2.96)	25.61	13.52	53.70	0.25
EL	54.36	8.91	28.61	0.66	1.53	0.43
NKRE	47.56	0.66	43.80	0.64	0.73	0.88
NKR	69.26	6.13	27.29	0.34	10.17	0.03
YLd	56.96	6.17	27.7	44028.06	129557.4	0.34

AD = days to 50% anthesis, SD = days to 50% silking, ASI = anthesis-silking interval, MSD = maize streak disease, PH = plant height, EH = ear height, PlAsp = plant aspect, E rot = ear rot, EL = ear length, NKR = number of kernels row⁻¹, NKRE = number of kernel rows ear⁻¹ and YLd = grain yield kg /ha

Genetic Parameters

Estimates of variance due to general combining ability and specific combining ability are given in Table 4. The results showed that $\sigma^2_{gca}/\sigma^2_{sca}$ ratio was less than unity for days to 50% silking, maize streak disease, plant height, ear height, plant aspect, husk cover, ear rot, ear length, number of kernel rows ear⁻¹, number of kernels row⁻¹ and grain yield. On the other hand, $\sigma^2_{gca}/\sigma^2_{sca}$ ratio was higher than unity for days to 50% anthesis and anthesis-silking interval.

Estimate of Combining Ability Effects of Lines and Crosses for Different Traits

General Combining Abilities

Information on general combining ability effects of lines together with higher mean performance increases the chance of getting desirable hybrids.

Estimates of general combining ability effects for grain yield revealed both negative and positive GCA values, an indication that there were good and poor general combiners among lines for the traits studied. Inbreds L16, L1 and L8 exhibited good general combining ability effects and would be useful in maize breeding programmes for grain yield improvement as these lines have a genetic potential to transfer desirable traits to their progenies. From this study, the magnitude of GCA effect of the two testers was equal but opposite in sign. Tester CML 444 (T2) showed positive and significant GCA effect for grain yield. The current investigation is in agreement with the findings of several authors who reported both negative and positive combining ability effects for grain yield (Gichuru & Njoroge, 2011; Mhike *et al.*, 2011)

GCA estimates for days to 50% anthesis showed both negative and positive effects. The negative values indicate that there is a possibility to generate early flowering hybrids among crosses between these inbred lines. L8 (-3.88) and L5 (-1.38) were found to be good combiners for days to 50% anthesis and could be used for improvement of earliness in a breeding programme. In breed lines L3 (2.38) and L1 (1.38) were poor general combiners for days to anthesis which meant that they had delayed anthesis. Tester 1368 manifested negative GCA value and significant effects for days to anthesis. Similar findings have been reported by many investigators (Abrha *et al.*, 2013; Hosana *et al.*, 2015; Legesse *et al.*, 2009)

Estimates of GCA for days to 50% silking showed both negative and positive GCA values. Inbred lines L8 (-3.69) and L9 (-1.44) were found to be good general combiners for days to 50% silking. The negative sign is an indication of earliness and this is useful for the improvement of earliness. Tester 1368 showed negative GCA value but was not significant effect.

Similarly, GCA values for anthesis-silking interval (ASI) manifested both negative and positive GCA estimation. Negative GCA values for this trait implied that the female and male parents emerged silk and shed pollen, respectively nearly at the same time, which is good for synchronization. However, the positive GCA values for this trait indicate that, there were delays in days to 50% silking, which could result in lack of synchronization thereby affecting pollination and subsequently fertilization. Tester CML 444 had significant negative GCA effect for anthesis-silking interval. Findings from Abrha *et al.*, (2013); and Hosana *et al.*, (2015) who reported both negative and positive values for anthesis and silking is in agreement with the current investigation.

GCA estimates for maize streak virus disease revealed both negative and positive GCA values. L7 (-0.62) and L8 (-0.48) were found to be the best general combiners for MSV disease. Negative GCA values indicate the ability of inbred lines to transmit genes for resistance against MSV disease to the progenies. Positive GCA values for this trait imply that the inbred lines are susceptible to the MSV disease and therefore transmit genes for susceptibility to their progenies. Thus, GCA estimates indicated the possibility to select inbred lines that can be combined to generate hybrids that are resistant to MSV disease. This investigation is similar with previous findings by Gichuru & Njoroge, (2011).

Estimates of GCA for plant height showed both negative and positive GCA values. L10 (-20), L7 (-11), L6 (-10) and L3 (-9) were found to be good general combiners whereas L5 (14), L11 (12), L4 (8) and L13 (7) were found to be poor general combiners. In a maize breeding programme, shorter plants are needed to reduce the lodging problem. This means that the shorter plant will have less stem lodging problem. Similarly, GCA estimates detected both positive and negative GCA effect for ear height. L10 (-11), L6 (-8), L14 (-7.45) and L3 (-6) were found to be good general combiners with significant effects whereas, L1 (10), L16 (9), L13 (6) and L2 (6) showing poor general combining ability effects for ear height. Inbred lines with negative GCA values were good general combiner for plant height and ear height whereas, positive GCA effect showed poor general combining ability effect for plant height and ear height. Therefore, the result showed that there are inbred lines, which can be used for the improvement of traits in the desired direction. Several researchers have reported both negative and positive GCA estimates for these traits (Abrha *et al.*, 2013; Aguiar *et al.*, 2003; Silva *et al.*, 2010; Hosana *et al.*, 2015; Legesse *et al.*, 2009).

Estimates of GCA for plant aspect were both negative and positive for this trait. L8 (-0.97) and L12 (-0.72) were found to be good general combiners whereas L10 (1.03) and L15 (0.78) were found to be poor combiners. Negative or low GCA estimates for plant aspect imply that plants had a good performance such as free or less disease occurrence, uniform ear height and good grain filling. Thus, the result indicated the existence of a good inbred line that can be used as breeding material for the need of good plant aspect in future maize breeding.

GCA estimates for husk cover showed both negative and positive values with most of the inbred lines having negative GCA estimates. Inbred lines L8 (-8), L6 (-7) and L16 (-7) were found to be good combiners with significant negative GCA effects while L1 (23), L13 (19) and L14 (8) were found to be poor general combiners. Negative GCA values for husk cover are desirable for protection from bird attack, rain, ear rot and other yield loss factors. Thus, lines, which showed negative GCA values, can be used for the enhancement of husk cover in maize breeding programme. Similarly, GCA estimates for ear rots revealed both negative and positive GCA effects. Negative or low GCA effects indicate that the ears were not damaged by ear rots. Therefore, inbred lines with negative GCA values for ear rots should be used in the breeding programme to reduce yield loss due to ear rot. The reduction of ear rot infections is also important because it results in the reduction of mycotoxins in the grain making it safer for consumption (Munkvold *et al.*, 1997). Similar to the current finding negative and positive GCA effects for husk cover were reported by (Hosana *et al.*, 2015).

Estimates of GCA for ear length showed both negative and positive GCA values, showing that inbred lines with positive GCA values for ear length taking into consideration other yield characters have an implication for increasing yield of the progenies when crosses is made among lines with positive GCA estimates. Inbred lines L12, L1 and L5 found to be good general combiners for this trait.

GCA effect for number of kernel rows ear⁻¹ recorded both negative and positive GCA values. L16 (2.08) and L2 (1.83) were the best general combiners for number of kernel rows ear⁻¹. These inbred lines can be used in maize breeding

programme in the future. Most of the time positive GCA value for number of kernel rows ear⁻¹ is desirable for the increment of grain yield. It means that ears with higher kernel rows will give high grain yield. However, sometimes increased number of rows ear⁻¹ may result in small seeds, which may reduce yield.

Similarly, estimates of GCA for number of kernels row⁻¹ showed both negative and positive GCA effects. L12 (4.98), L5 (3.98),

L1 (3.23) and L8 (2.73) were found to be good general combiners and showed significant GCA effects for number of kernels row⁻¹. Positive GCA estimation value is desirable for the improvement of grain yield while negative GCA effects for the same trait is undesirable in maize breeding programme. This result is in accordance with the finding of Al-falahy, (2015); Divan *et al.*, (2013); Hosana *et al.*, (2015) ; and Pavan and Prakash, (2016).

Estimation of Specific Combining Ability (SCA)

The result for SCA estimates detected both negative and positive SCA values for a line crossed with the two testers with equal SCA values in magnitude and opposite in sign but varied with characters. This may due to the two testers, which had equal combining ability in magnitude but opposite in sign.

Estimates of SCA for grain yield: L8 x T2, L1 x T2, L16 x T1, L16 x T2, L4 x T2, and L9 x T1 were identified as the best specific combiners. These top specific crosses will be further tested for the improvement of productivity of maize grain yield by exploiting maximum heterosis. On the contrary, crosses with negative SCA values are undesirable for grain yield. However, to get the best SCA results is not necessarily from crosses between two good general combiners. From this study, it was found that the combination of a parent with negative and a parent with positive GCA value resulted in a hybrid with positive SCA values in some cases. For example, the combination of a parent with negative and a parent with positive GCA values L14 (-817) x T2 (256), L3 (-595) x T2 (256), L16 (867) x T1 (-256), resulted in positive SCA values of, 723, 621, 569 respectively. The combination of parents with positive and negative GCA values resulting in positive SCA values is in agreement with the reports from previous investigators (Zoran *et al.*, 2012). On the other hand, there were combinations of both parents with positive GCA values, which, resulted in hybrids with negative SCA values, L5 x T2, L7 x T2, L9 x T2, L13 x T2, L15 x T2 and L16 x T2. The reverse is also true where two parents with negative GCA values were crossed and gave hybrids with positive SCA values, such as L6 x T1 and L10 x T1. Therefore, from this study it was found that the good specific combiners for different traits involved parents with high x high, high x low, low x low general combining ability. The proportional contribution of variance due to lines was higher than the interaction of line by testers to the total variance of crosses and the contribution of variance due line by tester was higher than the testers. Days to 50% silking, plant and ear height, ear length, number of kernel rows ear⁻¹, and grain yield exhibited significant GCA and SCA effects; however, the $\sigma^2_{gca}/\sigma^2_{sca}$ ratios were less than unity, indicating that non-additive genetic variance played a greater role in controlling the inheritance of these traits. This finding is in agreement with several researchers (Abrha *et al.*, 2013; Liaqat *et al.*, 2015; Muhammad *et al.*, 2010; Oyekunle *et al.*, 2013).

SCA estimates for days to 50% silking showed both negative and positive SCA effects. Negative SCA estimates for this trait indicate that the crosses took fewer days to 50% silking. This implies that crosses with negative SCA values can be used for development of varieties with earliness. On the contrary, crosses, which had positive SCA estimates for days to 50% silking can be selected to develop late flowering hybrids for areas, which have long rainy seasons. The current investigation is similar with previous reports (Abrha *et al.*, 2013; Hosana *et al.*, 2015; Mhike *et al.*, 2011).

Estimates of SCA effects for plant and ear height revealed both negative and positive SCA estimates. The negative SCA value indicates that the possibility to shorten the plant height and ear height to reduce stem lodging problems in maize and for ease of mechanized operations. The current finding is similar with the previous investigation (Mhike *et al.*, 2011).

The significant and negative SCA effect observed for husk cover in L1 x T2, L3 x T2, L10 x T2 and L13 x T1 is an indication that these crosses had no plants with poor husk cover. These specific crosses can be used in maize breeding programmes to improve poor husk cover and to protect grains from birds, rains, ear rot and insects. Similar results were reported by previous authors (Hosana *et al.*, 2015).

The five testcrosses that had significant positive SCA effect for ear length can be used in a heterosis-breeding programme to develop high yielding maize varieties. Thus, longer ears are desirable and can result in higher grain yield. Estimates of SCA for number of kernel rows ear⁻¹ revealed six best positive specific combiners in the desired direction. Positive SCA estimates indicate that there were higher numbers of kernel rows ear⁻¹, which can contribute to increase in grain yield in the cross. Similarly, estimation of SCA for number of kernel row⁻¹, 10 testcrosses among 32 crosses revealed positive and significant SCA effects. Similar findings of the current work has been reported by several researchers (Divan *et al.*, 2013; Hosana *et al.*, 2015 ; Rahman *et al.*, 2013).

CONCLUSIONS AND RECOMMENDATIONS

This study was conducted with the overall objective of investigating combining ability of tropical white maize inbred lines. Line x tester analysis identified inbred lines with good GCA and best single crosses combinations with desirable SCA for the characters studied. Significant differences for lines and testcrosses were detected for different traits studied, which indicated that both additive and non-additive gene action played a role in controlling in the inheritance of most traits, which means both progeny selection and heterosis breeding will be effective for future breeding programme. However, $\sigma^2_{gca}/\sigma^2_{sca}$ ratio was less than unity for days to 50% silking, plant and ear height, ear length, number of kernel rows ear⁻¹, number of kernels row⁻¹ and grain yield, which indicated the preponderance of non-additive gene action in governing the inheritance of these traits in the hybrids. There was larger proportional contribution of GCA effects of female inbred lines for grain yield and yield contributing characters than those of SCA effects to the total sum of squares variance of crosses.

In general, information generated on combining ability should be used to find best maize breeding strategy for developing high yielding white maize lines and hybrids.

Table 4: Estimate of General Combining Ability (GCA) Effect of Lines and Testers for Studied Traits of Tropical white Maize in Line X Tester Mating Fashion (16 x 2) at University of Ghana, WACCI Research Farm (2015/16)

Lines	AD	SD	ASI	MSD	PH	EH	PLASP	HC (%)	E rot%
1	1.38***	1.81***	0.42	0.31	3.21	10.35**	0.03	22.91***	0.32**
2	0.88*	0.81*	-0.08	0.02	2.31	6.3*	-0.47	-6.34	-0.15
3	2.38***	1.56***	-0.83**	0.12	-8.84**	-5.75*	0.28	4.66	0.10
4	0.13	0.31	0.17	0.18	8.46**	4.55	-0.47	-2.09	-0.07
5	-1.38***	-1.19***	0.17	-0.23	14.01***	1.1	0.28	-3.34	-0.17
6	-1.13**	0.06	1.42***	0.24	-10.39***	-8.35**	0.28	-6.59*	-0.11
7	0.88*	0.56	-0.33	-0.62**	-11.09***	-5.1	0.03	-4.59	-0.30**
8	-3.88***	-3.69***	0.17	-0.48**	2.36	2.2	-0.97***	-8.09*	-0.30**
9	-1.13**	-1.44***	-0.33	-0.32	-0.04	1.2	-0.22	-3.09	-0.18
10	0.88*	0.56	-0.33	0.37*	-19.64***	-11.05***	1.03***	-0.59	0.19
11	-1.13**	-0.94**	0.17	-0.35*	11.61***	-2.15	-0.21	-4.34	-0.09

Table 4: Contd.,									
12	0.63	0.31	-0.33	0.02	-1.19	1.8	-0.72**	-4.59	0.13
13	1.13**	0.81*	-0.33	-0.35*	6.51*	6.4*	0.28	18.69**	0.11
14	0.38	0.56	0.17	0.31	-1.24	-7.45*	0.53*	7.91*	0.12
15	-0.38	-0.94**	-0.57*	0.52**	2.16	-2.85	0.78**	-3.84	0.09
16	0.38	0.81*	0.42	0.09	1.86	8.8*	-0.47	-6.59*	-0.19
GCASE	0.36	0.32	0.26	0.17	2.74	2.81	0.23	3.21	0.11
SE(gi-gj)	0.51	0.45	0.42	0.23	3.99	3.92	0.31	4.95	0.16
T1	-0.31**	-0.09	0.23**	0.01	1.17	-2.76***	0.31***	1.03	-0.02
T2	0.31**	0.09	-0.23**	-0.01	-1.17	2.76***	-0.31***	-1.03	0.02
GCASE	0.09	0.08	0.07	0.04	0.71	0.73	0.06	0.83	0.03
SE (gi-gj)	0.18	0.16	0.15	0.08	1.41	1.38	0.11	1.75	0.37

*, ** and ***, $P \leq 0.05$, $P \leq 0.01$ and $P \leq 0.001$, respectively.

- T1 = tester 1368 and T2 = tester CML 444.
- GCA value of the two testers was equal in magnitude but opposite in sign AD = days to 50% anthesis, SD = days to 50% silking, ASI = days to anthesis-silking intervals, MSD = maize streak disease scored, PH = plant height, EH = ear height, pl ASP = plant aspect, HC% = husk cover in percent, E rot = ear rot in percent

Table 4: Continued

Lines	EL	NKRE	NKR	Yld kg ha ⁻¹
1	1.77***	-0.17	3.23**	595.33*
2	0.77	1.83**	1.73	295.72
3	-1.23**	0.83	-3.77**	-594.96*
4	0.02	-0.42	0.23	11.22
5	1.02*	0.83	3.98**	181.44
6	0.02	-2.17***	-0.77	-522.95*
7	0.27	-0.17	1.73	105.30
8	-0.23	-1.17*	2.73*	549.73*
9	-0.23	0.83	-0.02	246.73
10	-2.73***	-1.17*	-5.02***	-996.23***
11	-2.98***	0.58	-5.27***	-201.23
12	3.52***	-1.67*	4.98***	-268.84
13	0.51	0.33	-0.52	260.87
14	-0.48	0.33	-2.77*	-817.39***
15	-0.73	-0.67	0.48	288.31
16	0.77	2.08***	-1.02	866.95***
GCASE	0.42	0.50	1.12	223.39
SE (gi-gj)	0.63	0.69	1.67	329.20
T1	-0.55 ***	-0.36**	0.30	-256.22***
T2	0.55***	0.36**	-0.30	256.22***
GCASE	0.11	0.13	0.30	57.67
SE (gi-gj)	0.22	0.24	0.59	116.39

EL = ear length, NKRE = number of kernel rows ear⁻¹, NKR = number of kernels row⁻¹ and Yld kg

ha⁻¹ = grain yield kg ha⁻¹

Table 5: Estimation of Specific Combining Ability (SCA) Effects of Testcrosses for the Studied Traits of Tropical White Maize in a Line X Tester ((16 x 2) Mating Fashion at University of Ghana, WACCI Research Farm (2015/-16)

Cross	SD	PH	EH	EL	NKRE ⁻¹	NKR ⁻¹	Yld kg/ha
L1 x T1	0.09	12.03***	1.36	-0.2	-0.64	1.80	-491*
L1 x T2	-0.09	-12.03***	-1.36	0.2	0.64	-1.80	491*
L2 x T1	0.09	6.13*	5.21	-0.2	0.36	-0.20	163
L2 x T2	-0.09	-6.13*	-5.21	0.2	-0.36	0.20	-163
L3 x T1	0.84*	-8.62**	-11.84***	-0.2	0.36	-2.20	-620**
L3 x T2	-0.84*	8.62**	11.84***	0.2	-0.36	2.20	620**

Table 5: Contd.,

L4 x T1	-0.41	1.98	6.06*	-1.95***	-0.39	-6.20***	-214
L4 x T2	0.41	-1.98	-6.06*	1.95***	0.39	6.20***	214
L5 x T1	0.09	-0.47	-1.69	0.05	1.36**	0.05	109
L5 x T2	-0.09	0.47	1.69	-0.05	-1.36**	-0.05	-109
L6 x T1	-0.66*	6.63*	7.56**	0.55	-0.64	1.30	424
L6 x T2	0.66*	-6.63*	-7.56***	-0.55	0.64	-1.30	-424
L7 x T1	-0.66*	2.93	5.71*	0.3	0.36	-0.70	442
L7 x T2	0.66*	-2.93	-5.71*	-0.3	-0.35	0.70	-442
L8 x T1	0.59	-6.52*	-5.79*	-0.7	-0.64	-1.70	-903***
L8 x T2	-0.59	6.52*	5.79*	0.7	0.64	1.70	903***
L9 x T1	-0.66*	-3.92	-2.59	0.3	0.36	0.55	476*
L9 x T2	0.66*	3.92	2.59	-0.3	-0.36	-0.55	-476*
L10 x T1	0.34	-11.31***	-5.84*	2.30***	-0.64	4.55***	174
L10 x T2	-0.34	11.32***	5.84*	-2.30***	0.64	-4.55***	-174
L11 x T1	0.34	0.23	-3.84	3.05***	1.11*	5.30***	-137
L11 x T2	-0.34	-0.23	3.84	-3.05***	-1.11*	-5.30***	137
L12 x T1	0.09	-8.07**	-1.99	0.55	-1.14*	2.05	176
L12 x T2	-0.09	8.07**	1.99	-0.55	1.14*	-2.05	-176
L13 x T1	0.09	7.03*	7.51*	-1.45**	0.86	-2.45*	233
L13 x T2	-0.09	-7.03*	-7.51*	1.45**	-0.86	2.45*	-233
L14 x T1	0.84*	-11.92**	-5.24	-0.45	-1.14*	-2.20	-723**
L14 x T2	-0.84*	11.92***	5.24	0.45	1.14*	2.20	723**
L15 x T1	-1.66***	13.88***	5.76*	-1.70***	1.86***	-3.45**	322
L15 x T2	1.66***	-13.88***	-5.76*	1.70***	-1.86***	3.45**	-322
L16 x T1	0.59	-0.02	-0.39	-0.2	-1.39**	3.55**	569*
L16 x T2	-0.59	0.02	0.39	0.2	1.39**	-3.55**	-569*
SCASE	0.32	2.74	2.81	0.42	0.50	1.12	223
SE(Sij-Ski)	0.64	5.64	5.54	0.89	0.97	2.36	466

*= $p \leq 0.05$, **= $P \leq 0.01$ and ***= $p \leq 0.001$.

T1= tester one (1368), T2= tester two (CML 444)

SD = days to 50% silking, PH = plant height, EH = ear height, EL= ear length, NKRE = number of kernels row ear⁻¹, NKR = number of kernels row⁻¹ and Yld kg ha⁻¹ = yield kilogram ha⁻¹

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